

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=6; day=24; hr=9; min=1; sec=31; ms=129; ]

=====

\*\*\*\*\*

Reviewer Comments:

For SEQ ID # 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, and 45, please reorder the numeric identifiers so the <300> series features come after all of the <200> series features.

For SEQ ID # 4, 6, 8, and 11, please remove the space found between the amino acids and the numbering.

For example in SEQ ID # 4:

Gly	Asp	Val	Phe	Thr	Met	Pro	Glu	Asp	Asp	Tyr	Trp	Ser	Tyr	Asp	Tyr
65					70					75					80

Val	Glu	Glu	Pro	Lys	Asn	Asn	Thr	Asn	Thr	Gly	Val	Gln	Pro	Glu	Asn
				85					90					95	

Thr	Ser	Pro	Pro	Gly	Asp	Leu	Asn	Pro	Arg	Thr	Asp	Gly	Thr	Leu	Lys
			100					105					110		

Remove the space between the amino acids and the numbers 85, 90, and 95. Look at the lines above and below for the correct format.

\*\*\*\*\*

Application No: 10587756 Version No: 1.0

Input Set:

Output Set:

Started: 2008-05-28 19:35:20.833  
 Finished: 2008-05-28 19:35:27.281  
 Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 448 ms  
 Total Warnings: 3  
 Total Errors: 62  
 No. of SeqIDs Defined: 46  
 Actual SeqID Count: 46

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (4)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (6)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (6)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (8)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 13 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 15 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 17 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 19 )
W 402	Undefined organism found in <213> in SEQ ID (21)

Output Set:

```

Started:      2008-05-28 19:35:20.833
Finished:    2008-05-28 19:35:27.281
Elapsed:     0 hr(s) 0 min(s) 6 sec(s) 448 ms
Total Warnings: 3
Total Errors: 62
No. of SeqIDs Defined: 46
Actual SeqID Count: 46

```

[illegible]

**Input Set:**

**Output Set:**

**Started:** 2008-05-28 19:35:20.833  
**Finished:** 2008-05-28 19:35:27.281  
**Elapsed:** 0 hr(s) 0 min(s) 6 sec(s) 448 ms  
**Total Warnings:** 3  
**Total Errors:** 62  
**No. of SeqIDs Defined:** 46  
**Actual SeqID Count:** 46

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 29 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 31 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 33 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 35 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 37 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 39 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 41 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 43 )
E 249	Order Sequence Error <313> -> <220>; Expected Mandatory Tag: <400> in SEQID ( 45 )
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
E 250	Structural Validation Error; Sequence listing may not be indexable

# SEQUENCE LISTING

<110> Miyake, Masato  
Yoshikawa, Tomohiro  
Mikyake, Jun

<120> EVENT SEQUENCES

<130> 690121.409USPC

<140> US 10/587,756

<141> 2005-01-27

<150> PCT/JP2005/001151

<151> 2005-01-27

<150> JP 2004-24923

<151> 2004-01-30

<160> 46

<170> PatentIn version 3.1

<210> 1

<211> 1929

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1929)

<223> fibronectin 1

<400> 1

atg ctt agg ggt ccg ggg ccc ggg ctg ctg ctg ctg gcc gtc cag tgc	48
Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys	
1 5 10 15	

ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag	96
Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln	
20 25 30	

gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc	144
Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser	
35 40 45	

aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa cag	192
Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln	
50 55 60	

tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat gga	240
Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly	
65 70 75 80	

gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag act	288
Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr	

85	90	95	
tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act tat			336
Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr			
100	105	110	
gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg gct			384
Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala			
115	120	125	
ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa ggg			432
Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly			
130	135	140	
ggg cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag act			480
Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr			
145	150	155	160
ggg ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga gaa			528
Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu			
165	170	175	
tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct ggg			576
Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly			
180	185	190	
act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc tgg			624
Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp			
195	200	205	
atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc act			672
Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr			
210	215	220	
tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc tat			720
Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr			
225	230	235	240
aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg ctc			768
Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu			
245	250	255	
cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag agg			816
Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg			
260	265	270	
cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc gat			864
His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp			
275	280	285	
gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct ccc			912
Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro			
290	295	300	
tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg atg			960
Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met			
305	310	315	320

cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc ctg	1008
Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu	
325 330 335	
ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac ggt	1056
Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly	
340 345 350	
ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat ggc	1104
Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly	
355 360 365	
agg acg gac agc aca act tcg aat tat gag cag gac cag aaa tac tct	1152
Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser	
370 375 380	
ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc	1200
Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser	
385 390 395 400	
aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac	1248
Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr	
405 410 415	
act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg	1296
Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly	
420 425 430	
acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg	1344
Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met	
435 440 445	
gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc	1392
Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg	
450 455 460	
att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg	1440
Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg	
465 470 475 480	
tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac	1488
Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr	
485 490 495	
tcg cag ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg	1536
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val	
500 505 510	
aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt	1584
Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys	
515 520 525	
aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac	1632
Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp	
530 535 540	

caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca	1680
Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser	
545 550 555 560	
tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc	1728
Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly	
565 570 575	
cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc	1776
Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser	
580 585 590	
tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc	1824
Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro	
595 600 605	
aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc	1872
Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser	
610 615 620	
aag tac att ctc agg tgg aga cct gtg agt atc cca ccc aga aac ctt	1920
Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu	
625 630 635 640	
gga tac tga	1929
Gly Tyr	
<210> 2	
<211> 642	
<212> PRT	
<213> Homo sapiens	
<400> 2	
Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys	
1 5 10 15	
Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln	
20 25 30	
Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser	
35 40 45	
Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln	
50 55 60	
Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly	
65 70 75 80	
Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr	



85

90

95

Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
 100 105 110

Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
 115 120 125

Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
 130 135 140

Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
 145 150 155 160

Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
 165 170 175

Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly  
 180 185 190

Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp  
 195 200 205

Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr  
 210 215 220

Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr  
 225 230 235 240

Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu  
 245 250 255

Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg  
 260 265 270

His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp  
 275 280 285

Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro  
 290 300

Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met

305		310		315		320
Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu						
	325		330		335	
Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly						
	340		345		350	
Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly						
	355		360		365	
Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser						
	370		375		380	
Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser						
	385		390		395	400
Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr						
	405		410		415	
Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly						
	420		425		430	
Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met						
	435		440		445	
Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg						
	450		455		460	
Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg						
	465		470		475	480
Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr						
	485		490		495	
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val						
	500		505		510	
Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys						
	515		520		525	
Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp						
	530		535		540	

Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser  
 545 550 555 560

Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly  
 565 570 575

Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser  
 580 585 590

Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro  
 595 600 605

Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser  
 610 615 620

Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu  
 625 630 635 640

Gly Tyr

<210> 3  
 <211> 1437  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)..(1437)  
 <223> vitronectin

<400> 3  
 atg gca ccc ctg agg ccc ttt ttc ata cta gcc ctg gtg gca tgg gtt 48  
 Met Ala Pro Leu Arg Pro Phe Phe Ile Leu Ala Leu Val Ala Trp Val  
 1 5 10 15  
 tct ctg gct gac caa gag tca tgc aag ggc cgc tgc act cag ggt ttc 96  
 Ser Leu Ala Asp Gln Glu Ser Cys Lys Gly Arg Cys Thr Gln Gly Phe  
 20 25 30  
 atg gcc agc aag aag tgt cag tgt gac gag ctt tgc act tac tat cag 144  
 Met Ala Ser Lys Lys Cys Gln Cys Asp Glu Leu Cys Thr Tyr Tyr Gln  
 35 40 45  
 agc tgc tgt gcc gac tac atg gag cag tgc aag ccc caa gta acg cgg 192  
 Ser Cys Cys Ala Asp Tyr Met Glu Gln Cys Lys Pro Gln Val Thr Arg  
 50 55 60

ggg	gac	gtg	ttc	act	atg	cca	gag	gat	gat	tat	tgg	agc	tat	gac	tac	240
Gly	Asp	Val	Phe	Thr	Met	Pro	Glu	Asp	Asp	Tyr	Trp	Ser	Tyr	Asp	Tyr	
65					70					75					80	
gtg	gag	gag	ccc	aag	aac	aat	acc	aac	acc	ggg	gtg	caa	ccc	gag	aac	288
Val	Glu	Glu	Pro	Lys	Asn	Asn	Thr	Asn	Thr	Gly	Val	Gln	Pro	Glu	Asn	
				85					90					95		
acc	tct	cca	ccc	ggg	gac	cta	aat	cct	cgg	acg	gac	ggc	act	cta	aag	336
Thr	Ser	Pro	Pro	Gly	Asp	Leu	Asn	Pro	Arg	Thr	Asp	Gly	Thr	Leu	Lys	
			100					105					110			
ccg	aca	gcc	ttc	cta	gat	cct	gag	gaa	cag	cca	agc	acc	cca	gcg	cct	384
Pro	Thr	Ala	Phe	Leu	Asp	Pro	Glu	Glu	Gln	Pro	Ser	Thr	Pro	Ala	Pro	
		115					120					125				
aaa	gtg	gag	caa	cag	gag	gag	atc	cta	agg	ccc	gac	acc	act	gat	caa	432
Lys	Val	Glu	Gln	Gln	Glu	Glu	Ile	Leu	Arg	Pro	Asp	Thr	Thr	Asp	Gln	
	130					135					140					
ggg	acc	cct	gag	ttt	cca	gag	gaa	gaa	ctg	tgc	agt	gga	aag	ccc	ttt	480
Gly	Thr	Pro	Glu	Phe	Pro	Glu	Glu	Glu	Leu	Cys	Ser	Gly	Lys	Pro	Phe	
145					150					155					160	
gac	gcc	ttc	acg	gat	ctc	aag	aat	ggg	tcc	ctc	ttt	gcc	ttc	cga	ggg	528
Asp	Ala	Phe	Thr	Asp	Leu	Lys	Asn	Gly	Ser	Leu	Phe	Ala	Phe	Arg	Gly	
				165					170					175		
cag	tac	cgc	tgt	gag	cta	gat	gag	acg	gca	gtg	agg	cct	ggg	tac	ccc	576
Gln	Tyr	Arg	Cys	Glu	Leu	Asp	Glu	Thr	Ala	Val	Arg	Pro	Gly	Tyr	Pro	
			180					185					190			
aaa	ctt	atc	caa	gat	gtc	tgg	ggc	att	gag	ggc	ccc	atc	gat	gct	gcc	624
Lys	Leu	Ile	Gln	Asp	Val	Trp	Gly	Ile	Glu	Gly	Pro	Ile	Asp	Ala	Ala	
		195					200					205				
ttc	act	cgc	atc	aac	tgt	cag	ggg	aag	acc	tac	ttg	ttc	aag	ggg	agt	672
Phe	Thr	Arg	Ile	Asn	Cys	Gln	Gly	Lys	Thr	Tyr	Leu	Phe	Lys	Gly	Ser	
	210					215					220					
cag	tac	tgg	cgc	ttt	gag	gat	ggg	gtc	ctg	gac	cct	ggg	tat	ccc	cga	720
Gln	Tyr	Trp	Arg	Phe	Glu	Asp	Gly	Val	Leu	Asp	Pro	Gly	Tyr	Pro	Arg	
225					230					235					240	
aac	atc	tcc	gaa	ggc	ttc	agt	ggc	ata	cca	gac	aat	gtt	gat	gca	gcg	768
Asn	Ile	Ser	Glu	Gly	Phe	Ser	Gly	Ile	Pro	Asp	Asn	Val	Asp	Ala	Ala	
				245					250					255		
ttc	gcc	ctt	cct	gcc	cac	cgt	tac	agt	ggc	cgg	gaa	agg	gtc	tac	ttc	816
Phe	Ala	Leu	Pro	Ala	His	Arg	Tyr	Ser	Gly	Arg	Glu	Arg	Val	Tyr	Phe	
			260					265					270			
ttc	aag	ggg	aag	cag	tac	tgg	gag	cac	gaa	ttt	cag	cag	caa	ccc		

cag gag gag tgc gaa ggc agc tct ctg tca gcc gtg ttt gag cac ttt	912
Gln Glu Glu Cys Glu Gly Ser Ser Leu Ser Ala Val Phe Glu His Phe	
290 295 300	
gcc ttg ctt cag cgg gac agc tgg gag aac att ttc gaa ctc ctc ttc	960
Ala Leu Leu Gln Arg Asp Ser Trp Glu Asn Ile Phe Glu Leu Leu Phe	
305 310 315 320	
tgg ggc aga tcc tct gat gga gcc aga gaa ccc caa ttc atc agc cgg	1008
Trp Gly Arg Ser Ser Asp Gly Ala Arg Glu Pro Gln Phe Ile Ser Arg	
325 330 335	
aac tgg cat ggt gtg cca ggg aaa gtg gac gct gct atg gcc ggc cgc	1056
Asn Trp His Gly Val Pro Gly Lys Val Asp Ala Ala Met Ala Gly Arg	
340 345 350	
atc tac gtc act ggc tcc tta tcc cac tct gcc caa gcc aaa aaa cag	1104
Ile Tyr Val Thr Gly Ser Leu Ser His Ser Ala Gln Ala Lys Lys Gln	
355 360 365	
ccg tct aag cgt aga agc cga aag cgc tat cgt tca cgc cga ggg cgt	1152
Pro Ser Lys Arg Arg Ser Arg Lys Arg Tyr Arg Ser Arg Arg Gly Arg	
370	